

#2

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/006,366

DATE: 12/17/2001
TIME: 11:09:46

Input Set : A:\RTS-0332 Sequence Listing.txt
Output Set: N:\CRF3\12172001\J006366.raw

ENTERED

6 <110> APPLICANT: C. Frank Bennett
7 Kenneth W. Dobie
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF MHC CLASS II TRANSACTIVATOR

EXPRESSION

11 <130> FILE REFERENCE: RTS-0332
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/006,366
C--> 13 <141> CURRENT FILING DATE: 2001-11-05
13 <160> NUMBER OF SEQ ID NOS: 98
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 20
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
23 <223> OTHER INFORMATION: Antisense Oligonucleotide
25 <400> SEQUENCE: 1
26 tccgtcatcg ctccctcaggg
29 <210> SEQ ID NO: 2
30 <211> LENGTH: 20
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
36 <223> OTHER INFORMATION: Antisense Oligonucleotide
38 <400> SEQUENCE: 2
39 atgcattctg cccccaaggaa
42 <210> SEQ ID NO: 3
43 <211> LENGTH: 6672
44 <212> TYPE: DNA
45 <213> ORGANISM: Homo sapiens
47 <220> FEATURE:
49 <221> NAME/KEY: CDS
50 <222> LOCATION: (139)...(3531)
52 <400> SEQUENCE: 3
53 cctcccaact ggtgactgt tagtgatgag gctgtgtgct tctgagctgg gcatccgaag 60
54 gcatccttgg ggaagctgag ggcacgagga ggggtctgca gactccggaa gctgtgcct 120
55 ggctgggatt cttacaca atg cgt tgc ctg gtc cca cgc cct gct ggg tcc 171
56 Met Arg Cys Leu Ala Pro Arg Pro Ala Gly Ser
57 1 5 10
59 tac ctg tca gag ccc caa ggc agc tca cag tgc gtc acc atg gag ttg 219
60 Tyr Leu Ser Glu Pro Gln Gly Ser Ser Gln Cys Ala Thr Met Glu Leu
61 15 20 25
63 ggg ccc cta gaa ggt ggc tac ctg gag ctt ctt aac agc gat gct gac 267
64 Gly Pro Leu Glu Gly Tyr Leu Glu Leu Leu Asn Ser Asp Ala Asp
65 30 35 40
67 ccc ctg tgc ctc tac cac ttc tat gac cag atg gac ctg gct gga gaa 315
68 Pro Leu Cys Leu Tyr His Phe Tyr Asp Gln Met Asp Leu Ala Gly Glu
69 45 50 55
71 gaa gag att gag ctc tac tca gaa ccc gac aca gac acc atc aac tgc 363
72 Glu Glu Ile Glu Leu Tyr Ser Glu Pro Asp Thr Asp Thr Ile Asn Cys

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73	60	65	70	75	411
75	gac cag ttc agc agg ctg ttg tgt gac atg gaa ggt gat gaa gag acc				
76	Asp Gln Phe Ser Arg Leu Leu Cys Asp Met Glu Gly Asp Glu Glu Thr				
77	80	85	90		459
79	agg gag gct tat gcc aat atc gcg gaa ctg gac gag tat gtc ttc cag				
80	Arg Glu Ala Tyr Ala Asn Ile Ala Glu Leu Asp Gln Tyr Val Phe Gln				
81	95	100	105		507
83	gac tcc cag ctg gag ggc ctg agc aag gac att ttc aag cac ata gga				
84	Asp Ser Gln Leu Glu Gly Leu Ser Lys Asp Ile Phe Lys His Ile Gly				
85	110	115	120		555
87	cca gat gaa gtg atc ggt gag agt atg gag atg cca gca gaa gtt ggg				
88	Pro Asp Glu Val Ile Gly Glu Ser Met Glu Met Pro Ala Glu Val Gly				
89	125	130	135		603
91	cag aaa agt cag aaa aga ccc ttc cca gag gag ctt ccg gca gac ctg				
92	Gln Lys Ser Gln Lys Arg Pro Phe Pro Glu Glu Leu Pro Ala Asp Leu				
93	140	145	150	155	651
95	aag cac tgg aag cca gct gag ccc act gtg gtg act ggc agt ctc				
96	Lys His Trp Lys Pro Ala Glu Pro Pro Thr Val Val Thr Gly Ser Leu				
97	160	165	170		699
99	cta gtg gga cca gtg agc gac tgc tcc acc ctg ccc tgc ctg cca ctg				
100	Leu Val Gly Pro Val Ser Asp Cys Ser Thr Leu Pro Cys Leu Pro Leu				
101	175	180	185		747
103	cct gcg ctg ttc aac cag gag cca gcc tcc ggc cag atg cgc ctg gag				
104	Pro Ala Leu Phe Asn Gln Glu Pro Ala Ser Gly Gln Met Arg Leu Glu				
105	190	195	200		795
107	aaa acc gac cag att ccc atg cct ttc tcc agt tcc tcc tgg agc tgc				
108	Lys Thr Asp Gln Ile Pro Met Pro Phe Ser Ser Ser Leu Ser Cys				
109	205	210	215		843
111	ctg aat ctc cct gag gga ccc atc cag ttt gtc ccc acc atc tcc act				
112	Leu Asn Leu Pro Glu Gly Pro Ile Gln Phe Val Pro Thr Ile Ser Thr				
113	220	225	230	235	891
115	ctg ccc cat ggg ctc tgg caa atc tct gag gct gga aca ggg gtc tcc				
116	Leu Pro His Gly Leu Trp Gln Ile Ser Glu Ala Gly Thr Gly Val Ser				
117	240	245	250		939
119	agt ata ttc atc tac cat ggt gag gtg ccc gag gcc agc caa gta ccc				
120	Ser Ile Phe Ile Tyr His Gly Glu Val Pro Gln Ala Ser Gln Val Pro				
121	255	260	265		987
123	cct ccc agt gga ttc act gtc cac ggc ctc cca aca tct cca gac cgg				
124	Pro Pro Ser Gly Phe Thr Val His Gly Leu Pro Thr Ser Pro Asp Arg				
125	270	275	280		1035
127	cca ggc tcc acc acc ccc ttc gct cca tcc gcc act gac ctg ccc agc				
128	Pro Gly Ser Thr Ser Pro Phe Ala Pro Ser Ala Thr Asp Leu Pro Ser				
129	285	290	295		1083
131	atg cct gaa cct gcc ctg acc tcc cga gca aac atg aca gag cac aag				
132	Met Pro Glu Pro Ala Leu Thr Ser Arg Ala Asn Met Thr Glu His Lys				
133	300	305	310	315	1131
135	acg tcc ccc acc caa tgc ccc gca gct gga gag gtc tcc aac aag ctt				
136	Thr Ser Pro Thr Gln Cys Pro Ala Ala Gly Glu Val Ser Asn Lys Leu				
137	320	325	330		

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139 cca aaa tgg cct gag ccc gtc gag cag ttc tac cgc tca ctg cag gag	1179
140 Pro Lys Trp Pro Glu Pro Val Glu Gln Phe Tyr Arg Ser Leu Gln Asp	
335 340 345	
141	
143 acg tat ggt gcc gag ccc gca ggc ccc gat ggc atc cta gtg gag gtg	1227
144 Thr Tyr Gly Ala Glu Pro Ala Gly Pro Asp Gly Ile Leu Val Glu Val	
355 360	
145	
147 gat ctg gtg cag gcc agg ctg gag agg agc agc aag agc ctg gag	1275
148 Asp Leu Val Gln Ala Arg Leu Glu Arg Ser Ser Lys Ser Leu Glu	
365 370 375	
149	
151 cgg gaa ctg gcc acc ccc gac tgg gca gaa cgg cag ctg gcc caa gga	1323
152 Arg Glu Leu Ala Thr Pro Asp Trp Ala Glu Arg Gln Leu Ala Gln Gly	
385 390 395	
153 380	
155 ggc ctg gct gag gtg ctg ttg gct gcc aag gag cac cgg cgg cgt	1371
156 Gly Leu Ala Glu Val Leu Leu Ala Ala Lys Glu His Arg Arg Pro Arg	
400 405 410	
157	
159 gag aca cga gtg att gtg ctg ggc aaa gct ggt cag ggc aag agc	1419
160 Glu Thr Arg Val Ile Ala Val Leu Gly Lys Ala Gly Gln Gly Lys Ser	
415 420 425	
161	
163 tat tgg gct ggg gca gtg agc cgg gcc tgg gct tgt ggc cgg ctt ccc	1467
164 Tyr Trp Ala Gly Ala Val Ser Arg Ala Trp Ala Cys Gly Arg Leu Pro	
430 435 440	
165	
167 cag tac gac ttt gtc ttc tct gtc ccc tgc cat tgc ttg aac cgt ccc	1515
168 Glu Tyr Asp Phe Val Phe Ser Val Pro Cys His Cys Leu Asn Arg Pro	
445 450 455	
169	
171 ggg gat gcc tat ggc ctg cag gat ctg ctc ttc ctg ggc cca cag	1563
172 Gly Asp Ala Tyr Gly Leu Gln Asp Leu Leu Ser Leu Gly Pro Gln	
460 465 470 475	
173 460	
175 cca ctc gtg ggc ggc gat gag gtt ttc agc cac atc ttg aag aga cct	1611
176 Pro Leu Val Ala Ala Asp Glu Val Phe Ser His Ile Leu Lys Arg Pro	
480 485 490	
177	
179 gac cgc gtt ctg ctc atc cta gac gcc ttc gag gag ctg gaa ggc caa	1659
180 Asp Arg Val Leu Leu Ile Leu Asp Ala Phe Glu Leu Glu Ala Gln	
495 500 505	
181	
183 gat ggc ttc ctg cac agc acg tgc gga ccc gca ccc gag ccc tgc	1707
184 Asp Gly Phe Leu His Ser Thr Cys Gly Pro Ala Pro Ala Glu Pro Cys	
510 515 520	
185	
187 tcc ctc cgg ggg ctg ctc gcc ggc ctt ttc cag aag aag ctg ctc cga	1755
188 Ser Leu Arg Gly Leu Leu Ala Gly Leu Phe Glu Lys Lys Leu Leu Arg	
525 530 535	
189	
191 ggt tgc acc ctc ctc aca gcc cgg ccc egg ggc ccc ctc gtc gtc cag	1803
192 Gly Cys Thr Leu Leu Thr Ala Arg Pro Arg Gly Arg Leu Val Gln	
540 545 550 555	
193	
195 agc ctg agc aag gcc gac gcc cta ttt gag ctg tcc ggc ttc tcc atg	1851
196 Ser Leu Ser Lys Ala Asp Ala Leu Phe Glu Leu Ser Gly Phe Ser Met	
560 565 570	
197	
199 gag cag gcc cag gca tac gtg atg cgc tac ttt gag agc tca ggg atg	1899
200 Glu Gln Ala Gln Ala Tyr Val Met Arg Tyr Phe Glu Ser Ser Gly Met	
575 580 585	
201	
203 aca gag cac caa gac aga gcc ctg acg ctc ctc cgg gac cgg cca ctt	1947

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204	Thr	Glu	His	Gln	Asp	Arg	Ala	Leu	Thr	Leu	Leu	Arg	Asp	Arg	Pro	Leu	
205																590	
																595	
																600	
207	ctt	ctc	agt	cac	acg	cac	acg	cct	act	ttg	tgc	cgg	gca	gtg	tgc	cag	
208	Leu	Leu	Ser	His	Ser	His	Ser	Pro	Thr	Leu	Cys	Arg	Ala	Val	Cys	Gln	
209																605	
																610	
																615	
211	ctc	tca	gag	gcc	ctg	ctg	gag	ctt	ggg	gag	gac	gcc	aag	ctg	ccc	tcc	
212	Leu	Ser	Glu	Ala	Leu	Leu	Glu	Leu	Gly	Glu	Asp	Ala	Lys	Leu	Pro	Ser	
213																620	
																625	
																630	
215	acg	ctc	acg	gga	ctc	tat	gtc	ggc	ctg	ggc	cgt	gca	gcc	ctc	gac		
216	Thr	Leu	Thr	Gly	Leu	Tyr	Val	Gly	Leu	Leu	Gly	Arg	Ala	Ala	Leu	Asp	
217																640	
																645	
219	agc	ccc	ccc	ggg	gcc	ctg	gca	gag	ctg	gcc	aag	ctg	gcc	tgg	gag	ctg	
220	Ser	Pro	Pro	Gly	Ala	Leu	Ala	Glu	Leu	Ala	Lys	Leu	Ala	Trp	Glu	Leu	
221																655	
																660	
																665	
223	ggc	cgc	aga	cat	caa	agt	acc	cta	cag	gac	cag	ttc	cca	tcc	gca		
224	Gly	Arg	Arg	His	Gln	Ser	Thr	Leu	Glu	Asp	Gln	Phe	Pro	Ser	Ala		
225																670	
																680	
227	gac	gtg	agg	acc	tgg	ggc	atg	gcc	aaa	ggc	tta	gtc	caa	cac	cca	ccg	
228	Asp	Val	Arg	Thr	Trp	Ala	Met	Ala	Lys	Gly	Leu	Val	Gln	His	Pro	Pro	
229																685	
																690	
																695	
231	cg	ggc	gca	gag	tcc	gtc	ctg	gcc	ttc	ccc	agg	ttc	ctc	ctg	caa	tgc	
232	Arg	Ala	Ala	Glu	Ser	Glu	Leu	Ala	Phe	Pro	Ser	Phe	Leu	Gln	Cys		
233																700	
																705	
																710	
235	tcc	ctg	ggg	gcc	ctg	tgg	ctg	gtc	gtt	agg	ggc	gaa	atc	aag	gac	aag	
236	Phe	Leu	Gly	Ala	Leu	Trp	Leu	Ala	Leu	Ser	Gly	Glu	Ile	Lys	Asp	Lys	
237																720	
																725	
																730	
239	gag	ctc	ccg	tac	cta	gca	ttt	acc	cca	agg	aag	agg	agg	ccc	tat		
240	Glu	Leu	Pro	Gln	Tyr	Leu	Ala	Leu	Thr	Pro	Arg	Lys	Lys	Arg	Pro	Tyr	
241																735	
																740	
																745	
243	gac	aac	tgg	ctg	gag	ggc	gtc	cca	cg	tcc	ttt	ctg	gtc	atc	tcc		
244	Asp	Asn	Trp	Leu	Glu	Gly	Val	Pro	Arg	Phe	Leu	Ala	Gly	Ile	Ile	Phe	
245																750	
																755	
																760	
247	cag	cct	ccc	gcc	ccg	tgc	ctg	gg	gcc	cta	ctc	ggg	cca	tcc	ggc	gtc	
248	Gln	Pro	Pro	Ala	Arg	Cys	Leu	Gly	Ala	Leu	Leu	Gly	Pro	Ser	Ala	Ala	
249																765	
																770	
																775	
251	gcc	tgc	gtg	gac	agg	aag	cag	aa	gtg	ctt	ggc	agg	tac	ctg	aag	ccg	
252	Ala	Ser	Val	Asp	Arg	Lys	Gln	Lys	Val	Leu	Ala	Arg	Tyr	Leu	Lys	Arg	
253																780	
																785	
																790	
255	ctg	cag	ccg	ggg	aca	ctg	ccg	gg	cgg	cag	ctt	gag	ctg	ctg	cac		
256	Leu	Gln	Pro	Gly	Thr	Leu	Arg	Ala	Arg	Gln	Leu	Leu	Glu	Leu	Leu	His	
257																800	
																805	
																810	
259	tgc	gcc	cac	gag	gcc	gag	gag	gct	gga	att	tgg	cac	gtc	gtt	aa	ccg	
260	Cys	Ala	His	Glu	Ala	Glu	Ala	Glu	Gly	Ile	Trp	Gln	His	Val	Val	Gln	
261																815	
																820	
																825	
263	gag	ctc	ccc	gcc	ccg	ctc	tct	ttt	ctg	ggc	acc	ccg	ctc	acg	cct	cct	
264	Glu	Leu	Pro	Gly	Arg	Leu	Ser	Ph	Leu	Gly	Thr	Arg	Leu	Thr	Pro	Pro	
265																830	
																835	
																840	
267	gat	gca	cat	gtt	ctg	ggc	aag	gcc	ttt	gag	ggc	gca	ggc	caa	gac	tcc	
268	Asp	Ala	His	Val	Leu	Gly	Lys	Ala	Leu	Glu	Ala	Gly	Gln	Asp	Phe		

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269	845	850	855	2763														
271	tcc	ctg	gac	ctc	cgc	agc	act	ggc	att	tgc	ccc	tct	gga	ttg	ggg	agc	2763	
272	Ser	Leu	Asp	Leu	Arg	Ser	Thr	Gly	Ile	Cys	Pro	Ser	Gly	Leu	Gly	Ser	875	
273	860	865	870	875														
275	ctc	gtg	gga	ctc	agc	tgt	gtc	acc	cgt	tgc	agg	gtc	gcc	ttg	agc	gac	2811	
276	Leu	Val	Gly	Leu	Ser	Cys	Val	Thr	Arg	Phe	Arg	Ala	Ala	Leu	Ser	Asp	890	
277	880	885	890	2859														
279	acg	gtg	ggc	ctg	tgg	gag	tcc	ctg	cgg	cag	cat	ggg	gag	acc	aag	cta	2859	
280	Thr	Val	Ala	Leu	Leu	Trp	Glu	Ser	Leu	Arg	Gln	His	Gly	Glu	Thr	Lys	Leu	2859
281	895	900	905	2907														
283	ctt	cag	gca	gca	gca	gag	gag	aag	ttc	acc	atc	gac	gat	cct	aaa	gcc	aag	2907
284	Leu	Gln	Ala	Ala	Ala	Glu	Glu	Lys	Phe	Thr	Ile	Glu	Pro	Phe	Lys	Ala	Lys	2907
285	910	915	920	2955														
287	tcc	ctg	aag	gat	gtg	gaa	gac	ctg	gga	aag	ctt	gtg	cag	act	cag	agg	2955	
288	Ser	Leu	Lys	Asp	Val	Glu	Asp	Leu	Gly	Lys	Leu	Val	Gln	Thr	Gln	Arg	2955	
289	925	930	935	3003														
291	acg	aga	aga	agt	tcc	tcg	gaa	gac	aca	gct	ggg	gag	atc	ccc	cct	gtc	gtt	2903
292	Thr	Arg	Ser	Ser	Ser	Glu	Asp	Thr	Ile	Ala	Gly	Glu	Leu	Pro	Ala	Val	Arg	2903
293	940	945	950	955	3051													
295	gac	tca	aag	aaa	ctg	gag	ttt	ggc	ctg	ggc	cct	gtc	tca	ggc	ccc	cag	3051	
296	Asp	Leu	Lys	Lys	Glu	Phe	Ala	Leu	Gly	Pro	Val	Ser	Gly	Pro	Gln	3051		
297	960	965	970	3099														
299	gct	ttc	ccc	aaa	ctg	gtg	cg	atc	ctc	acg	gcc	ttt	tcc	tcc	ctg	cag	3099	
300	Ala	Phe	Pro	Lys	Leu	Val	Arg	Ile	Leu	Thr	Ala	Phe	Ser	Ser	Leu	Gln	3099	
301	975	980	985	3147														
303	cat	ctg	gac	ctg	gtt	gag	gag	aac	atc	ggg	gac	gag	gtt	3147				
304	His	Leu	Asp	Leu	Asp	Ala	Leu	Ser	Glu	Asn	Lys	Ile	Gly	Asp	Glu	Gly	3147	
305	990	995	1000	3195														
307	gtc	tcg	cag	ctc	tca	gcc	acc	tcc	ccc	cag	atg	tcc	ttt	tcc	gaa	acc	3195	
308	Val	Ser	Gln	Leu	Ser	Ala	Thr	Phe	Pro	Gln	Leu	Lys	Ser	Leu	Glu	Thr	3243	
309	1005	1010	1015	3243														
311	ctc	aat	ctg	tcc	cag	aac	aat	atc	act	gac	ctg	gtt	gcc	tac	aaa	ctc	3243	
312	Leu	Asn	Leu	Ser	Gln	Asn	Asn	Ile	Thr	Asp	Leu	Gly	Ala	Tyr	Lys	Leu	3243	
313	1020	1025	1030	1035	3291													
315	gcc	gag	gcc	ctg	cct	tcg	ctc	gtc	gca	tcc	ttc	ctc	agg	cta	agc	ttg	3291	
316	Ala	Glu	Ala	Leu	Pro	Ser	Leu	Ala	Ala	Ser	Leu	Leu	Arg	Leu	Ser	Leu	3291	
317	1040	1045	1050	3339														
319	tac	aat	aac	tgc	atc	tgc	gac	gtt	ggg	gcc	gag	agc	ttg	gtt	cgt	gtg	3339	
320	Tyr	Asn	Asn	Cys	Ile	Cys	Asp	Val	Gly	Ala	Glu	Ser	Leu	Ala	Arg	Val	3339	
321	1055	1060	1065	3387														
323	ctt	ccg	gac	atg	gtg	tcc	ctc	cg	gtt	atg	gac	gtc	cag	tac	aac	aag	3387	
324	Leu	Pro	Asp	Met	Val	Ser	Leu	Arg	Val	Met	Asp	Val	Gln	Tyr	Asn	Lys	3387	
325	1070	1075	1080	3435														
327	ttc	acg	gtc	gcc	ggg	gcc	cag	cag	ctc	gtc	acc	gtc	ttt	ggg	agg	tgt	3435	
328	Phe	Thr	Ala	Ala	Gly	Ala	Gln	Gln	Leu	Ala	Ala	Ser	Leu	Arg	Arg	Cys	3435	
329	1085	1090	1095	3483														
331	cct	cat	gtg	gag	acg	ctg	gcy	atg	tgg	acg	ccc	acc	atc	cca	ttc	agt	3483	
332	Pro	His	Val	Glu	Thr	Leu	Ala	Met	Trp	Thr	Pro	Ile	Pro	Phe	Ser	3483		
333	1100	1105	1110	3483														

VERIFICATION SUMMARY
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:580 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14